SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Thomas, Lawrence J.

(ii) TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Banner & Witcoff, Ltd.
(B) STREET: 75 State Street, Suite 2300
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1807

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE WordPerfect 6.1

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: (not yet assigned)
(B) FILING DATE: 01 May 1997 (01.05.97)
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION: 08/640,713
(B) FILING DATE: 01 May 1996 (01.05.96)

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION: 08/802,967
(B) FILING DATE: 21 February 1997 (21.02.97)

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Leon R. Yankwich
(B) REGISTRATION NUMBER: 30,237
(C) REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872

(2) INFORMATION FOR SEQ ID NO: 1.
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE: Structural coding sequence for mature rabbit CETP
(A) NAME:
(B) LOCATION:
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Nagashima, Mariko, et al.

(B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
(C) JOURNAL: J. Lipid Res.
(D) VOLUME: 29
(E) ISSUE:
(F) PAGES: 1643 - 1649
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 T
1488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
TGTCCCAAAG GCGCCTCCTA CGAGGCTGGC ATCGTGTGTC GCATCACCAA      50
GCCCGCCCTC TTGGTGTTGA ACCAAGAGAC GGCCAAGGTG GTCCAGACGG     100
CCTTCCAGCG CGCCGGCTAT CCGGACGTCA GCGGCGAGAG GGCCGTGATG     150
CTCCTCGGCC GGGTCAAGTA CGGGCTGCAC AACCTCCAGA TCAGCCACCT     200
GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGACGCCAAG ACCATCGACG     250
TCGCCATCCA GAACGTGTCC GTGGTCTTCA AGGGGACCCT GAACTACAGC     300
TACACGAGTG CCTGGGGGTT GGGCATCAAT CAGTCTGTCG ACTTCGAGAT     350
CGACTCTGCC ATTGACCTCC AGATCAACAC AGAGCTGACC TGCGACGCTG     400
GCAGTGTGCG CACCAATGCC CCCGACTGCT ACCTGGCTTT CCATAAACTG     450
CTCCTGCACC TCCAGGGGGA GCGCGAGCCG GGGTGGCTCA AGCAGCTCTT     500
CACAAACTTC ATCTCCTTCA CCCTGAAGCT GATTCTGAAG GGACAGGTCT     550
GCAATGAGAT CAACACCATC TCCAACATCA TGGCTGACTT TGTCCAGACG     600
AGGGCCGCCA GCATCCTCTC AGATGGAGAC ATCGGGGTGG ACATTTCCGT     650
GACGGGGGCC CCTGTCATCA CAGCCACCTA CCTGGAGTCC CATCACAAGG     700
GTCACTTCAC GCACAAGAAC GTCTCCGAGG CCTTCCCCCT CCGCGCCTTC     750
CCGCCCGGTC TTCTGGGGGA CTCCCGCATG CTCTACTTCT GGTTCTCCGA     800
TCAAGTGCTC AACTCCCTGG CCAGGGCCGC CTTCCAGGAG GGCCGTCTCG     850
TGCTCAGCCT GACAGGGGAT GAGTTCAAGA AAGTGCTGGA GACCCAGGGT     900
TTCGACACCA ACCAGGAAAT CTTCCAGGAG CTTTCCAGAG GGCTTCCCAC     950
CGGCCAGGCC CAGGTAGCCG TCCACTGCCT TAAGGTGCCC AAGATCTCCT    1000
GCCAGAACCG GGGTGTCGTG GTGTCTTCTT CCGTCGCCGT GACGTTCCGC    1050
TTCCCCCGCC CAGATGGCCG AGAAGCTGTG GCCTACAGGT TTGAGGAGGA    1100
```

```
TATCATCACC ACCGTCCAGG CCTCCTACTC CCAGAAAAAG CTCTTCCTAC   1150
ACCTCTTGGA TTTCCAGTGC GTGCCGGCCA GCGGAAGGGC AGGCAGCTCA   1200
GCAAATCTCT CCGTGGCCCT CAGGACTGAG GCTAAGGCTG TTTCCAACCT   1250
GACTGAGAGC CGCTCCGAGT CCCTGCAGAG CTCTCTCCGC TCCCTGATCG   1300
CCACGGTGGG CATCCCGGAG GTCATGTCTC GGCTCGAGGT GGCGTTCACA   1350
GCCCTCATGA ACAGCAAAGG CCTGGACCTC TTCGAAATCA TCAACCCCGA   1400
GATTATCACT CTCGATGGCT GCCTGCTGCT GCAGATGGAC TTCGGTTTTC   1450
CCAAGCACCT GCTGGTGGAT TTCCTGCAGA GCCTGAGC                1488
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Amino acid sequence for mature rabbit CETP protein.
(B LOCATION:

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Nagashima, Mariko, et al.
(B) TITLE: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer protein
(C) JOURNAL: J. Lipid Res.
(D) VOLUME 29
(E) ISSUE:
(F) PAGES: 1643 - 1649
(G) DATE: 1988
(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys
1               5                   10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn Gln Glu
    15                  20                  25

Thr Ala Lys Val Val Gln Thr Ala Phe Gln Arg Ala Gly
            30                  35

Tyr Pro Asp Val Ser Gly Glu Arg Ala Val Met Leu Leu
```

```
40                  45                  50

Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile Ser
        55                  60                  65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp
                70                  75

Ala Lys Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val
    80                  85                  90

Val Phe Lys Gly Thr Leu Asn Tyr Ser Tyr Thr Ser Ala
            95                  100

Trp Gly Leu Gly Ile Asn Gln Ser Val Asp Phe Glu Ile
105                 110                 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu Leu Thr
        120                 125                 130

Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys
                135                 140

Tyr Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly
    145                 150                 155

Glu Arg Glu Pro Gly Trp Leu Lys Gln Leu Phe Thr Asn
            160                 165

Phe Ile Ser Phe Thr Leu Lys Leu Ile Leu Lys Arg Gln
170                 175                 180

Val Cys Asn Glu Ile Asn Thr Ile Ser Asn Ile Met Ala
        185                 190                 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
                200                 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro
    210                 215                 220

Val Ile Thr Ala Thr Tyr Leu Glu Ser His His Lys Gly
            225                 230

His Phe Thr His Lys Asn Val Ser Glu Ala Phe Pro Leu
235                 240                 245

Arg Ala Phe Pro Pro Gly Leu Leu Gly Asp Ser Arg Met
        250                 255                 260

Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser Leu
                265                 270

Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser
    275                 280                 285

Leu Thr Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln
```

```
            290                 295

Gly Phe Asp Thr Asn Gln Glu Ile Phe Gln Glu Leu Ser
300                 305                 310

Arg Gly Leu Pro Thr Gly Gln Ala Gln Val Ala Val His
        315                 320                 325

Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn Arg Gly
                330                 335

Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe
    340                 345                 350

Pro Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe
            355                 360

Glu Glu Asp Ile Ile Thr Thr Val Gln Ala Ser Tyr Ser
365                 370                 375

Gln Lys Lys Leu Phe Leu His Leu Leu Asp Phe Gln Cys
        380                 385                 390

Val Pro Ala Ser Gly Arg Ala Gly Ser Ser Ala Asn Leu
                395                 400


Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
    405                 410                 415

Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu
            420                 425

Arg Ser Leu Ile Ala Thr Val Gly Ile Pro Glu Val Met
430                 435                 440

Ser Arg Leu Glu Val Ala Phe Thr Ala Leu Met Asn Ser
        445                 450                 455

Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu Ile
                460                 465

Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe
    470                 475                 480

Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser
            485                 490

Leu Ser
495
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1428 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Structural coding sequence for mature human CETP
(B) LOCATION:
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Drayna, Dennis, et al.
(B) TITLE: Cloning and sequencing of human cholesteryl ester transfer cDNA
(C) JOURNAL: Nature
(D) VOLUME: 327
(E) ISSUE:
(F) PAGES: 632 - 634
(G) DATE: 18-JUN-1987
(K) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
TGCTCCAAAG GCACCTCGCA CGAGGCAGGC ATCGTGTGCC GCATCACCAA    50

GCCTGCCCTC CTGGTGTTGA ACCACGAGAC TGCCAAGGTG ATCCAGACCG   100

CCTTCCAGCG AGCCAGCTAC CCAGATATCA CGGGCGAGAA GGCCATGATG   150

CTCCTTGGCC AAGTCAAGTA TGGGTTGCAC AACATCCAGA TCAGCCACTT   200

GTCCATCGCC AGCAGCCAGG TGGAGCTGGT GGAAGCCAAG TCCATTGATG   250

TCTCCATTCA GAACGTGTCT GTGGTCTTCA AGGGGACCCT GAAGTATGGC   300

TACACCACTG CCTGGTGGCT GGGTATTGAT CAGTCCATTG ACTTCGAGAT   350

CGACTCTGCC ATTGACCTCC AGATCAACAC ACAGCTGACC TGTGACTCTG   400

GTAGAGTGCG GACCGATGCC CCTGACTGCT ACCTGTCTTT CCATAAGCTG   450

CTCCTGCATC TCCAAGGGGA GCGAGAGCCT GGGTGGATCA AGCAGCTGTT   500

CACAAATTTC ATCTCCTTCA CCCTGAAGCT GGTCCTGAAG GGACAGATCT   550

GCAAAGAGAT CAACGTCATC TCTAACATCA TGGCCGATTT TGTCCAGACA   600

AGGGCTGCCA GCATCCTTTC AGATGGAGAC ATTGGGGTGG ACATTTCCCT   650

GACAGGTGAT CCCGTCATCA CAGCCTCCTA CCTGGAGTCC CATCACAAGG   700

GTCATTTCAT CTACAAGAAT GTCTCAGAGG ACCTCCCCCT CCCCACCTTC   750

TCGCCCACAC TGCTGGGGGA CTCCCGCATG CTGTACTTCT GGTTCTCTGA   800

GCGAGTCTTC CACTCGCTGG CCAAGGTAGC TTTCCAGGAT GGCCGCCTCA   850

TGCTCAGCCT GATGGGAGAC GAGTTCAAGG CAGTGCTGGA GACCTGGGGC   900
```

```
TTCAACACCA ACCAGGAAAT CTTCCAAGAG GTTGTCGGCG GCTTTCCCAG    950

CCAGGCCCAA GTCACCGTCC ACTGCCTCAA GATGCCCAAG ATCTCCTGCC   1000

AAAACAAGGG AGTCGTGGTC AATTCTTCAG TGATGGTGAA ATTCCTCTTT   1050

CCACGCCCAG ACCAGCAACA TTCTGTAGCT TACACATTTG AAGAGGATAT   1100

CGTGACTACC GTCCAGGCCT CCTATTCTAA GAAAAAGCTC TTCTTAAGCC   1150

TCTTGGATTT CCAGATTACA CCAAAGACTG TTTCCAACTT GACTGAGAGC   1200

AGCTCCGAGT CCATCCAGAG CTTCCTGCAG TCAATGATCA CCGCTGTGGG   1250

CATCCCTGAG GTCATGTCTC GGCTCGAGGT AGTGTTTACA GCCCTCATGA   1300

ACAGCAAAGG CGTGAGCCTC TTCGACATCA TCAACCCTGA GATTATCACT   1350

CGAGATGGCT TCCTGCTGCT GCAGATGGAC TTTGGCTTCC CTGAGCACCT   1400

GCTGGTGGAT TTCCTTCAGA GCTTGAGC                           1428


(2)  INFORMATION FOR SEQ ID NO: 4:
     (i)    SEQUENCE CHARACTERISTICS:
            (A) LENGTH:   476 amino acids
            (B) TYPE:     amino acid
            (D) TOPOLOGY:    linear
     (ii)   MOLECULE TYPE:   peptide
     (iii)  HYPOTHETICAL:
     (iv)   ANTI-SENSE:
     (ix)   FEATURE:
            (A) NAME:     Amino acid sequence of mature human
                          CETP
            (B) LOCATION:
     (x)    PUBLICATION INFORMATION:
            (A) AUTHORS:  Drayna, Dennis, et al.
            (B) TITLE:    Cloning and sequencing of human
                          cholesteryl ester transfer cDNA
            (C) JOURNAL:  Nature
            (D) VOLUME:   327
            (E) ISSUE:
            (F) PAGES:    632 - 634
            (G) DATE:     18-JUN-1987
            (K) RELEVANT RESIDUES IN SEQ ID NO:4: FROM 1 TO
                                                  476


     (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys
1               5                   10

Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu
    15                  20                  25

Thr Ala Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser
```

```
            30                  35

Tyr Pro Asp Ile Thr Gly Glu Lys Ala Met Met Leu Leu
40                  45                  50

Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile Ser
        55                  60                  65

His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu
                70                  75

Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val
    80                  85                  90

Val Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Thr Ala
            95                  100

Trp Trp Leu Gly Ile Asp Gln Ser Ile Asp Phe Glu Ile
105                 110                 115

Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln Leu Thr
        120                 125                 130

Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys
                135                 140

Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly
    145                 150                 155

Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn
            160                 165

Phe Ile Ser Phe Thr Leu Lys Leu Val Leu Lys Gly Gln
170                 175                 180

Ile Cys Lys Glu Ile Asn Val Ile Ser Asn Ile Met Ala
        185                 190                 195

Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
                200                 205

Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro
    210                 215                 220

Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly
            225                 230

His Phe Ile Tyr Lys Asn Val Ser Glu Asp Leu Pro Leu
235                 240                 245

Pro Thr Phe Ser Pro Thr Leu Leu Gly Asp Ser Arg Met
        250                 255                 260

Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser Leu
                265                 270

Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser
    275                 280                 285
```

```
Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp
            290                 295

Gly Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val
300                 305                 310

Gly Gly Phe Pro Ser Gln Ala Gln Val Thr Val His Cys
        315                 320                 325


Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys Gly Val
                330                 335

Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro
    340                 345                 350

Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
            355                 360

Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys
365                 370                 375

Lys Lys Leu Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr
        380                 385                 390

Pro Lys Thr Val Ser Asn Leu Thr Glu Ser Ser Ser Glu
                395                 400

Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
    405                 410                 415

Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe
            420                 425

Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp
430                 435                 440

Ile Ile Asn Pro Glu Ile Ile Thr Arg Asp Gly Phe Leu
        445                 450                 455

Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His Leu Leu
                460                 465

Val Asp Phe Leu Gln Ser Leu Ser
    470                 475
```

(2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE:
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:

(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
GCGGCCGCCA TGCAGTACAT CAAGGCCAAC TCCAAGTTCA TCGGCATCAC    50

GGAGCGCTTC CCGCGCCCAG ATGGCCGAGA AGCTGTGGCC TACAGGTTTG   100

AGGAGGATAT CTTCGGTTTT CCCAAGCACC TGCTGGTGGA TTTCCTGCAG   150

AGCCTGAGCT AGCGGCCGC                                     169
```

(2) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
(ix) FEATURE:
(A) NAME: Complementary strand to SEQ ID NO:5
(B) LOCATION: 1 to 169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
GCGGCCGCTA GCTCAGGCTC TGCAGGAAAT CCACCAGCAG GTGCTTGGGA    50

AAACCGAAGA TATCCTCCTC AAACCTGTAG GCCACAGCTT CTCGGCCATC   100

TGGGCGCGGG AAGCGCTCCG TGATGCCGAT GAACTTGGAG TTGGCCTTGA   150

TGTACTGCAT GGCGGCCGC                                     169
```

(2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL:
(iv) ANTI-SENSE:
ix FEATURE: amino acid sequence of peptide encoded by bases 10 to 159 of SEQ ID NO:5
(A) NAME:
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
1               5                   10

Thr Glu Arg Phe Pro Arg Pro Asp Gly Arg Glu Ala Val
    15                  20                  25
```

Ala Tyr Arg Phe Glu Glu Asp Ile Phe Gly Phe Pro Lys
            30   35

His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
40   45   50

(2) INFORMATION FOR SEQ ID NO:8:
   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1608 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE:
   (iii) HYPOTHETICAL:
   (iv) ANTI-SENSE:
   (ix) FEATURE:
      (A) NAME: translational stop codon
      (B) LOCATION: 1606 - 1608

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCGCTGATG ATGTTGTTGA TTCTTCTAAA TCTTTTGTGA TGGAAAACTT 50

TTCTTCGTAC CACGGGACTA AACCTGGTTA TGTAGATTCC ATTCAAAAAG 100

GTATACAAAA GCCAAAATCT GGTACACAAG GAAATTATGA CGATGATTGG 150

AAAGGGTTTT ATAGTACCGA CAATAAATAC GACGCTGCGG GATACTCTGT 200

AGATAATGAA AACCCGCTCT CTGGAAAAGC TGGAGGCGTG GTCAAAGTGA 250

CGTATCCAGG ACTGACGAAG GTTCTCGCAC TAAAAGTGGA TAATGCCGAA 300

ACTATTAAGA AAGAGTTAGG TTTAAGTCTC ACTGAACCGT TGATGGAGCA 350

AGTCGGAACG GAAGAGTTTA TCAAAAGGTT CGGTGATGGT GCTTCGCGTG 400

TAGTGCTCAG CCTTCCCTTC GCTGAGGGGA GTTCTAGCGT TGAATATATT 450

AATAACTGGG AACAGGCGAA AGCGTTAAGC GTAGAACTTG AGATTAATTT 500

TGAAACCCGT GGAAAACGTG GCCAAGATGC GATGTATGAG TATATGGCTC 550

AAGCCTGTGC AGGAAATCGT GTCAGGCGAT CAGTAGGTAG CTCATTGTCA 600

TGCATAAATC TTGATTGGGA TGTCATAAGG GATAAAACTA AGACAAAGAT 650

AGAGTCTTTG AAAGAGCATG GCCCTATCAA AAATAAAATG AGCGAAAGTC 700

CCAATAAAAC AGTATCTGAG GAAAAAGCTA AACAATACCT AGAAGAATTT 750

CATCAAACGG CATTAGAGCA TCCTGAATTG TCAGAACTTA AAACCGTTAC 800

TGGGACCAAT CCTGTATTCG CTGGGGCTAA CTATGCGGCG TGGGCAGTAA 850

ACGTTGCGCA AGTTATCGAT AGCGAAACAG CTGATAATTT GGAAAAGACA 900

ACTGCTGCTC TTTCGATACT TCCTGGTATC GGTAGCGTAA TGGGCATTGC 950

AGACGGTGCC GTTCACCACA ATACAGAAGA GATAGTGGCA CAATCAATAG 1000

CTTTATCGTC TTTAATGGTT GCTCAAGCTA TTCCATTGGT AGGAGAGCTA 1050

GTTGATATTG GTTTCGCTGC ATATAATTTT GTAGAGAGTA TTATCAATTT 1100

ATTTCAAGTA GTTCATAATT CGTATAATCG TCCCGCGTAT TCTCCGGGGC 1150

ATAAAACGCA ACCATTTCTT CATGACGGGT ATGCTGTCAG TTGGAACACT 1200

GTTGAAGATT CGATAATCCG AACTGGTTTT CAAGGGGAGA GTGGGCACGA 1250

CATAAAAATT ACTGCTGAAA ATACCCCGCT TCCAATCGCG GGTGTCCTAC 1300

TACCGACTAT TCCTGGAAAG CTGGACGTTA ATAAGTCCAA GACTCATATT 1350

TTCGTAAATG GTCGGAAAAT AAGGATGCGT TGCAGAGCTA TAGACGGTGA 1400

TGTAACTTTT TGTCGCCCTA AATCTCCTGT TTATGTTGGT AATGGTGTGC 1450

ATGCGAATCT TCACGTGGCA TTTCACAGAA GCAGCTCGGA GAAAATTCAT 1500

TCTAATGAAA TTTCGTCGGA TTCCATAGGC GTTCTTGGGT ACCAGAAAAC 1550

```
AGTAGATCAC ACCAAGGTTA ATTCTAAGCT ATCGCTATTT TTTGAAATCA    1600

AAAGCTGA                                                  1608


(2)     INFORMATION FOR SEQ ID NO:9:
        (i)     SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 535 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear
        (ii)    MOLECULE TYPE: protein
        (iii)   HYPOTHETICAL:
        (iv)    ANTI-SENSE:
        (ix)    FEATURE:
                (A) NAME:
                    (B) LOCATION:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met
1               5                   10

Glu Asn Phe Ser Ser Tyr His Gly Thr Lys Pro Gly Tyr Val
15                  20                  25

Asp Ser Ile Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr
    30                  35                  40

Gln Gly Asn Tyr Asp Asp Asp Trp Lys Gly Phe Tyr Ser Thr
        45                  50                  55

Asp Asn Lys Tyr Asp Ala Ala Gly Tyr Ser Val Asp Asn Glu
            60                  65                  70

Asn Pro Leu Ser Gly Lys Ala Gly Gly Val Val Lys Val Thr
                75                  80

Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys Val Asp Asn
85                  90                  95

Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr Glu
    100                 105                 110

Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg
        115                 120                 125

Phe Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe
            130                 135                 140

Ala Glu Gly Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu
                145                 150

Gln Ala Lys Ala Leu Ser Val Glu Leu Glu Ile Asn Phe Glu
155                 160                 165

Thr Arg Gly Lys Arg Gly Gln Asp Ala Met Tyr Glu Tyr Met
```

```
    170                 175                 180

Ala Gln Ala Cys Ala Gly Asn Arg Val Arg Arg Ser Val Gly
        185                 190                 195

Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp Val Ile Arg
            200                 205                 210

Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His Gly
                215                 220

Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Asn Lys Thr Val
225                 230                 235

Ser Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln
    240                 245                 250

Thr Ala Leu Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val
        255                 260                 265

Thr Gly Thr Asn Pro Val Phe Ala Gly Ala Asn Tyr Ala Ala
            270                 275                 280

Trp Ala Val Asn Val Ala Gln Val Ile Asp Ser Glu Thr Ala
                285                 290

Asp Asn Leu Glu Lys Thr Thr Ala Ala Leu Ser Ile Leu Pro
295                 300                 305

Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly Ala Val His
    310                 315                 320

His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser
        325                 330                 335

Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu
            340                 345                 350

Val Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile
                355                 360

Ile Asn Leu Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro
365                 370                 375

Ala Tyr Ser Pro Gly His Lys Thr Gln Pro Phe Leu His Asp
    380                 385                 390

Gly Tyr Ala Val Ser Trp Asn Thr Val Glu Asp Ser Ile Ile
        395                 400                 405

Arg Thr Gly Phe Gln Gly Glu Ser Gly His Asp Ile Lys Ile
            410                 415                 420

Thr Ala Glu Asn Thr Pro Leu Pro Ile Ala Gly Val Leu Leu
                425                 430

Pro Thr Ile Pro Gly Lys Leu Asp Val Asn Lys Ser Lys Thr
435                 440                 445
```

```
His Ile Ser Val Asn Gly Arg Lys Ile Arg Met Arg Cys Arg
    450                 455                 460

Ala Ile Asp Gly Asp Val Thr Phe Cys Arg Pro Lys Ser Pro
        465                 470                 475

Val Tyr Val Gly Asn Gly Val His Ala Asn Leu His Val Ala
            480                 485                 490

Phe His Arg Ser Ser Ser Glu Lys Ile His Ser Asn Glu Ile
                495                 500

Ser Ser Asp Ser Ile Gly Val Leu Gly Tyr Gln Lys Thr Val
505                 510                 515

Asp His Thr Lys Val Asn Ser Lys Leu Ser Leu Phe Phe Glu
    520                 525                 530

Ile Lys Ser
        535


(2)     INFORMATION FOR SEQ ID NO:10
        (i)    SEQUENCE CHARACTERISTICS:
               (A)  LENGTH: 21 amino acids
               (B)  TYPE:  amino acid
               (D)  TOPOLOGY:  linear
        (ii)   MOLECULE TYPE:  protein
        (iii)  HYPOTHETICAL:
        (iv)   ANTI-SENSE:
        (ix)   FEATURE:
               (A)  NAME:
               (B)  LOCATION:

        (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO: 10:

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
1               5                   10


Lys Val Ser Ala Ser His Leu Glu
    15                  20
```